

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 1, 2004, 13:46:59 ; Search time 15 Seconds

(without alignments)
83.366 Million cell updates/sec

Title: US-09-674-616a-2

Perfect score: 67

Sequence: 1 NQEQQVSPYTLKQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 245

Minimum DB seq length: 13

Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PTR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match % | Length | DB | ID | Description |
|------------|-------|-------|---------|--------|--------|----|--|
| 1 | 20 | 29.9 | 13 | 2 | S47361 | | T-cell antigen receptor VJ junction beta chain - human |
| 2 | 29.9 | 13 | 2 | 29.6 | | | T-cell antigen receptor VJ junction beta chain - human |
| 3 | 28.4 | 13 | 2 | 32473 | | | T-cell antigen receptor VJ junction beta chain - human |
| 4 | 28.4 | 13 | 2 | PL0157 | | | T-cell antigen receptor VJ junction beta chain - human |
| 5 | 26.9 | 13 | 2 | BE1458 | | | T-cell antigen receptor VJ junction beta chain - human |
| 6 | 26.9 | 13 | 2 | BE1458 | | | T-cell antigen receptor VJ junction beta chain - human |
| 7 | 25.4 | 13 | 1 | UNBO | | | T-cell antigen receptor VJ junction beta chain - human |
| 8 | 25.4 | 13 | 2 | AA4818 | | | T-cell antigen receptor VJ junction beta chain - human |
| 9 | 25.4 | 13 | 2 | A53608 | | | T-cell antigen receptor VJ junction beta chain - human |
| 10 | 25.4 | 13 | 2 | A52050 | | | T-cell antigen receptor VJ junction beta chain - human |
| 11 | 25.4 | 13 | 2 | A61067 | | | T-cell antigen receptor VJ junction beta chain - human |
| 12 | 25.4 | 13 | 2 | A50174 | | | T-cell antigen receptor VJ junction beta chain - human |
| 13 | 25.4 | 13 | 2 | PT0256 | | | T-cell antigen receptor VJ junction beta chain - human |
| 14 | 23.9 | 13 | 2 | PC1149 | | | T-cell antigen receptor VJ junction beta chain - human |
| 15 | 23.9 | 13 | 2 | A61514 | | | T-cell antigen receptor VJ junction beta chain - human |
| 16 | 22.4 | 13 | 2 | S15755 | | | T-cell antigen receptor VJ junction beta chain - human |
| 17 | 22.4 | 13 | 2 | BE6093 | | | T-cell antigen receptor VJ junction beta chain - human |
| 18 | 22.4 | 13 | 2 | A54326 | | | T-cell antigen receptor VJ junction beta chain - human |
| 19 | 22.4 | 13 | 2 | BB8810 | | | T-cell antigen receptor VJ junction beta chain - human |
| 20 | 22.4 | 13 | 2 | S47358 | | | T-cell antigen receptor VJ junction beta chain - human |
| 21 | 22.4 | 13 | 2 | PH1599 | | | T-cell antigen receptor VJ junction beta chain - human |
| 22 | 20.9 | 13 | 2 | AB1361 | | | T-cell antigen receptor VJ junction beta chain - human |
| 23 | 20.9 | 13 | 2 | PT0038 | | | T-cell antigen receptor VJ junction beta chain - human |
| 24 | 20.9 | 13 | 2 | S56668 | | | T-cell antigen receptor VJ junction beta chain - human |
| 25 | 20.9 | 13 | 2 | S2471 | | | T-cell antigen receptor VJ junction beta chain - human |
| 26 | 20.9 | 13 | 2 | S2472 | | | T-cell antigen receptor VJ junction beta chain - human |
| 27 | 20.9 | 13 | 2 | DE1458 | | | T-cell antigen receptor VJ junction beta chain - human |
| 28 | 20.9 | 13 | 2 | ED1458 | | | T-cell antigen receptor VJ junction beta chain - human |
| 29 | 20.9 | 13 | 2 | S47362 | | | T-cell antigen receptor VJ junction beta chain - human |

ALIGNMENTS

RESULT 1
S47361
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47361
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-DR201 restricted recognition of influenza A is dominated by T cells
A;Reference number: S47361
A;Accession: S47361
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: EMBL:235685; NID:9527459; PIDN:CAA84754.1; PID:9527460
C;Keywords: T-cell receptor

RESULT 1
S47361
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47361
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-DR201 restricted recognition of influenza A is dominated by T cells
A;Reference number: S47361
A;Accession: S47361
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: EMBL:235685; NID:9527459; PIDN:CAA84754.1; PID:9527460
C;Keywords: T-cell receptor

Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conserv. 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.6e+03;
Matches 3; Conserv. 3; Mismatches 2; Indels 0; Gaps 0;

T-cell antigen receptor
conceptus protein
Ig H chain v-D-J r
T-cell receptor al
collecting duct wa
tubulin beta chain
phloroglucinol red
ribosomal protein
T-cell receptor be
mannose-1-phosphat
Ig heavy chain C r
Ig kappa chain J r
hypothetical prote
epithelial dog all

Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conserv. 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.6e+03;
Matches 3; Conserv. 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 3

S32473 Lynnaeapramide 3 - great pond snail
C;Species: *Lymnaea stagnalis* (great pond snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999

A;Accession: S32473
R;Johnson, A.H.; Rehfeld, J.F.
EUR. J. Biochem. 21, 875-879, 1993
A;Title: Lynnaeapramides, a new family of neuropeptides from the pond snail, *Lymnaea stagnalis*
A;Accession: S32473
A;Molecule type: protein
A;Residues: 1-13 <JOH>
A;Cross-references: PIDN:AB26364.1; PID:9299831
A;Experimental source: *glandula*
C;Keywords: amidated carboxyl end; neuropeptide
F;13/Modified site: amidated carboxyl end (phe) #status predicted

Query Match 20.4%; Score 19; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PYTRILKG 13
Db 1 PYDRISG 7

RESULT 4

PI0157 Ig kappa chain VII region (anti-myelin-associated glycoprotein, PSC) - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
C;Accession: PI0157; C01458
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-assoc
A;Reference number: A61458; MUID:90039128; PMID:2478651
A;Accession: PI0157
A;Molecule type: protein
A;Residues: 1-13 <BRO>
A;Accession: C01458
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <BR2>
C;Comment: This protein is one of monoclonal IgM reactive with myeloma-associated glycoprotein
C;Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 28.4%; Score 19; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 SPYTL 10
Db 7 SPVTL 11

RESULT 5

B61458 Ig kappa chain V-I region (BLA) - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C;Accession: B61458
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-assoc
A;Reference number: A61458; MUID:90039128; PMID:2478651
A;Accession: B61458
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <BRO>
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.9%; Score 18; DB 2; Length 13;

Qy 7 PYTL 10
Db 7 SPVTL 11

RESULT 6

A61458 Ig kappa chain V-I region (BLA) - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1995
C;Accession: A61458; PI0156
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-assoc
A;Reference number: A61458; MUID:90039128; PMID:2478651
A;Accession: A61458
A;Molecule type: protein
A;Residues: 1-13 <BRO>
C;Comment: This protein is one of monoclonal IgM reactive with myeloma-associated glycoprotein
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.9%; Score 18; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 SPYTL 10
Db 7 SPVTL 11

RESULT 7

UNBO neurotensin - bovine
C;Species: *Bos primigenius taurus* (cattle)
C;Accession: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Feb-1995
C;Accession: A01420
R;Carraway, R.; Leeman, S.E.
J. Biol. Chem. 250, 1917-1911, 1975
A;Title: The amino acid sequence of a hypothalamic peptide, neurotensin.
A;Reference number: A92172; MUID:75095678; PMID:1167549
A;Accession: A01420
A;Accession: A01420
A;Molecule type: protein
A;Residues: 1-13 <CAR>
A;Experimental source: hypothalamus
A;Reference number: A92173; MUID:75095679; PMID:1112938
A;Contents: annotation; synthesis
A;Note: a tripeptide chemically and pharmacologically identical with the natural peptide
C;Superfamily: neurotensin
C;Keywords: neurotensin; pyroglutamic acid (Gln) #status experimental
F;13/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
Db 10 PYTL 13

RESULT 8

A44818 extracellular lipase - *Pseudomonas aeruginosa* (fragment)
C;Species: *Pseudomonas aeruginosa*
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: A44818
R;Gilbert, E.J.; Cornish, A.; Jones, C.W.

Query Match

| | Db | 10 PYTL 13 |
|---|--|------------|
| QY | 6 SPYTLK 12 | |
| Db | 1 STYRQTK 7 | |
| RESULT 9 | | |
| A53608 | neurotensin - guinea pig | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) | | |
| C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 02-Sep-2000 | | |
| C;Accession: A53608 | | |
| R;Shaw, C.; Thim, L.; Conlon, J.M. | | |
| FEB5 Iett, 202, 187-191, 1986 | | |
| A;Title: [Ser(7)]neurotensin: isolation from guinea pig intestine. | | |
| A;Reference number: A53608; MUID:86248085; PMID:308775 | | |
| A;Status: preliminary | | |
| A;Molecule type: protein | | |
| A;Residues: 1-13 <SHA> | | |
| C;Superfamily: neurotensin | | |
| Query Match 25.4%; Score 17; DB 2; Length 13; | | |
| Best Local Similarity 57.1%; Pred. No. 5.9e+03; Mismatches 3; Indels 0; Gaps 0; | | |
| Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | |
| QY | 7 PYTL 10 | |
| Db | 10 PYTL 13 | |
| RESULT 10 | | |
| A28505 | neurotensin [validated] - chicken | |
| C;Species: <i>Galulus gallus</i> (chicken) | | |
| C;Accession: A28505 | | |
| R;Iwabuchi, H.; Komori, S.; Ohashi, H.; Kimura, S. | | |
| Jpn. J. Pharmacol. 44, 455-459, 1987 | | |
| A;Title: The amino acid sequence of a smooth muscle-contracting peptide from chicken rectum | | |
| A;Reference number: A28505; MUID:88063566; PMID:3682409 | | |
| A;Accession: A28505 | | |
| A;Molecule type: protein | | |
| A;Residues: 1-13 <IWA> | | |
| A;Experimental source: rectum | | |
| C;Comment: The peptide isolated from rectum is identical with chicken neurotensin and has a superfamily: neurotensin | | |
| C;Keywords: hormone; neuropeptide; pyroglutamic acid | | |
| F1-13-/Product: neurotensin #status experimental <NTS> | | |
| F1-/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental | | |
| Query Match 25.4%; Score 17; DB 2; Length 13; | | |
| Best Local Similarity 75.0%; Pred. No. 5.9e+03; Mismatches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | |
| QY | 7 PYTL 10 | |
| Db | 10 PYTL 13 | |
| RESULT 11 | | |
| A61067 | neurotensin - common frog | |
| C;Species: <i>Rana temporaria</i> (common frog) | | |
| C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Aug-1994 | | |
| C;Accession: A61067 | | |
| R;Shaw, C.; McKay, D.M.; Halton, D.W.; Thim, L.; Buchanan, K.D. | | |
| Regul. Pept. 38, 23-31, 1992 | | |
| A;Title: Isolation and primary structure of an amphibian neurotensin. | | |
| A;Reference number: A61067; MUID:92245104; PMID:1574601 | | |
| A;Molecule type: protein | | |
| A;Residues: 1-13 <SHA> | | |
| A;Note: this peptide was identified in brain, intestine, and rectum, but not in stomach | | |
| C;Superfamily: neurotensin | | |
| F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental | | |
| Query Match 25.4%; Score 17; DB 2; Length 13; | | |
| Best Local Similarity 75.0%; Pred. No. 5.9e+03; Mismatches 0; Mismatches 1; Indels 0; Gaps 0; | | |
| Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | |
| QY | 7 PYTL 10 | |
| Db | 10 PYTL 13 | |
| RESULT 12 | | |
| A05174 | tryptophyllin-13 - Röhde's leaf frog | |
| C;Species: <i>Phylomedusa rohdei</i> (Röhde's leaf frog) | | |
| C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000 | | |
| C;Accession: A05174 | | |
| R;Montecuccchi, P.C.; Gozzini, L.; Erispaner, V. | | |
| Int. J. Pept. Protein Res. 27, 175-182, 1986 | | |
| A;Reference number: A05174 | | |
| A;Accession: A05174 | | |
| A;Molecule type: protein | | |
| A;Residues: 1-13 <MON> | | |
| C;Superfamily: unassigned animal peptides | | |
| C;Keywords: pyroglutamic acid; skin | | |
| F1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental | | |
| Query Match 25.4%; Score 17; DB 2; Length 13; | | |
| Best Local Similarity 60.0%; Pred. No. 5.9e+03; Mismatches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| QY | 4 QVSPY 8 | |
| Db | 1 QEKPQY 5 | |
| RESULT 13 | | |
| PT0256 | Ig heavy chain CRD3 region (clone 2-115C) - human (fragment) | |
| C;Species: <i>Homo sapiens</i> (man) | | |
| C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996 | | |
| C;Accession: PT0256 | | |
| R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. | | |
| J. Exp. Med. 173, 395-407, 1991 | | |
| A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jcb1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental | | |
| A;Accession: PT0256 | | |
| A;Molecule type: DNA | | |
| A;Residues: 1-13 <YAM> | | |
| A;Experimental source: B lymphocyte | | |
| C;Keywords: heterotetramer; immunoglobulin | | |
| Query Match 25.4%; Score 17; DB 2; Length 13; | | |
| Best Local Similarity 50.0%; Pred. No. 5.9e+03; Mismatches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | |
| Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | |
| QY | 7 PYTL 10 | |

| Matches | 3; | Conservative | 1; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
|---------|----|--------------|----|------------|----|--------|----|------|----|
| QY | 8 | YTLIKG 13 | | | | | | | |
| | | : | | | | | | | |
| Db | 4 | YDMLTG 9 | | | | | | | |

RESULT 14

PC1149
 equinatoxin 1A - sea anemone (*Actinia equina*) (fragment)
 C;Species: *Actinia equina*
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PC1149
 R;Komatsu, S.; Furukawa, K.; Abe, K.; Hirano, H.; Ueda, M.
 Chem. Pharm. Bull. 40, 2873-2875, 1992
 A;Title: Isolation and characterization of equinatoxins from the sea anemone *Actinia equina*
 A;Reference number: PC1149; MUID:93099631; PMID:1361161
 A;Accession: PC1149
 A;Molecule type: protein
 A;Residues: 1-13 <KOM>
 C;Keywords: toxin

Query Match 23.9%; Score 16; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 9.1e+03; 1; Mismatches 0; Indels 0; Gaps 0;

| Matches | 3; | Conservative | 1; | Mismatches | 1; | Indels | 0; | Gaps | 0; |
|---------|----|--------------|----|------------|----|--------|----|------|----|
| QY | 1 | NDPEQV 5 | | | | | | | |
| | | : | | | | | | | |
| Db | 4 | NQAEV 8 | | | | | | | |

RESULT 15

A61514
 glutathione transferase (EC 2.5.1.18), 26k - fluke (*Schistosoma japonicum*) (fragment)
 C;Species: *Schistosoma japonicum*
 C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 07-May-1999
 C;Accession: A61514
 R;Mitchell, G.F.
 Mol. Biochem. Parasitol. 27, 249-256, 1988
 A;Title: Expression of an enzymatically active parasite molecule in *Escherichia coli*: Sc
 A;Reference number: A61514; MUID:88142994; PMID:3278228
 A;Accession: A61514
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <MIT>
 C;Keywords: transferase

Query Match 23.9%; Score 16; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 9.1e+03; 1; Mismatches 2; Indels 0; Gaps 0;

| Matches | 3; | Conservative | 1; | Mismatches | 2; | Indels | 0; | Gaps | 0; |
|---------|----|--------------|----|------------|----|--------|----|------|----|
| QY | 8 | YTLIKG 13 | | | | | | | |
| | | : | | | | | | | |
| Db | 6 | YWKIKG 11 | | | | | | | |

Search completed: October 1, 2004, 13:48:33
 Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 13:46:58 ; Search time 9 Seconds
(without alignments)
75.212 Million cell updates/sec

Title: US-09-674-616A-2
Perfect score: 67
Sequence: 1 NQEQVSPYTLKG 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 96

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------|---------------------|
| 1 | 20 | 29.9 | 13 | 1 IDHA_CANFA | P54835 canis famili |
| 2 | 19 | 28.4 | 13 | 1 CHEP_PARID | P42718 parapolybia |
| 3 | 19 | 28.4 | 13 | 1 NP3_LYMST | P80180 lymnaea sta |
| 4 | 18 | 26.9 | 13 | 1 FR12_PEA | P83435 pisum sativ |
| 5 | 17 | 25.4 | 13 | 1 NISUTT_BIFMA | P81795 bufo marini |
| 6 | 17 | 25.4 | 13 | 1 NEUTT_CAVPO | P32560 cavia porce |
| 7 | 17 | 25.4 | 13 | 1 NIUTT_CHICKO | P13724 gallus galli |
| 8 | 17 | 25.4 | 13 | 1 NIUTT_RANTE | P41536 rana tempor |
| 9 | 17 | 25.4 | 13 | 1 TFL13_PHRD | P04096 phyllocoetus |
| 10 | 16 | 23.9 | 13 | 1 PEDI_HYDRA | P80578 hydra atten |
| 11 | 16 | 23.9 | 13 | 1 PROX_ORYSA | P83647 oryza sativ |
| 12 | 16 | 23.9 | 13 | 1 SAKA_ONCMI | P82238 oncorhynchus |
| 13 | 16 | 23.9 | 13 | 1 SA2B_ONCMI | P82239 oncorhynchus |
| 14 | 15 | 22.4 | 13 | 1 ACT7_SOYBN | P15987 glycine max |
| 15 | 15 | 22.4 | 13 | 1 E121_LITRU | P82057 litoria rub |
| 16 | 15 | 22.4 | 13 | 1 E122_LITRU | P82058 litoria rub |
| 17 | 15 | 22.4 | 13 | 1 UN12_CLOPA | P81353 closidium |
| 18 | 15 | 22.4 | 13 | 1 UPS1_UFURIN | P82036 uproleia i |
| 19 | 14 | 20.9 | 13 | 1 BRK_PARID | P42717 parapolybia |
| 20 | 14 | 20.9 | 13 | 1 CRBL_VESMA | P17332 vespa manda |
| 21 | 14 | 20.9 | 13 | 1 MEL_MOC | P81532 microptilia |
| 22 | 14 | 20.9 | 13 | 1 NPL_LYMST | P80178 lymnaea sta |
| 23 | 14 | 20.9 | 13 | 1 NP2_LYMST | P80179 lymnaea sta |
| 24 | 14 | 20.9 | 13 | 1 SODM_CANFA | P54712 canis famili |
| 25 | 14 | 20.9 | 13 | 1 TEMC_RANTE | P56918 rana tempor |
| 26 | 14 | 20.9 | 13 | 1 YPE2_LACLC | P42021 lactococcus |
| 27 | 13 | 19.4 | 13 | 1 FBB_RABIT | P14478 oryctolagus |
| 28 | 13 | 19.4 | 13 | 1 PHGR_EUBOX | P57793 eubacterium |
| 29 | 13 | 19.4 | 13 | 1 UN10_CLOPA | P81345 clostridium |
| 30 | 12 | 17.9 | 13 | 1 CRBL_VESAN | P17233 vespa anali |
| 31 | 12 | 17.9 | 13 | 1 CRBL_VESCR | P01518 vespa crabr |
| 32 | 12 | 17.9 | 13 | 1 CRBL_VESKA | P12334 vespa xanth |
| 33 | 12 | 17.9 | 13 | 1 PSAE_PEA | P20118 pisum sativ |

ALIGNMENTS

RESULT 1
ID: IDHA_CANFA
ID: IDHA_CANFA STANDARD; PRT; 13 AA.
AC P54836;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DB Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (EC 1.1.1.41) (Isocitric dehydrogenase) [NAD+-specific ICDH] (Fragment)
DE IDH3A;
GN
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
[1]
RN
RP
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504912;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.",
RL Electrophoresis 18:2795-2802(1997)
CC -!- CATALYTIC ACTIVITY: Isocitrate + NAD(+) = 2-oxoglutarate + CO(2) + NADH.
CC -!- SUBUNIT: Heterooligomer of subunits alpha, beta, and gamma in the apparent ratio of 2:1:1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: Belongs to the isocitrate and isopropylmalate dehydrogenases family.
DR HSC-2DPAGE; P4836; DOG.
DR InterPro; IPR001804; Isodh.
DR PROSITE; PS00470; IDH_IMDH; PARTIAL.
KW Oxidoreductase; NAD; Tricarboxylic acid cycle; Mitochondrion.
FT NON_THR 13 13
SQ SEQUENCE 13 AA; 1356 MW; 9ABFBC2B2A34B2D1 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 QVSPLYTLKG 13
Dy 3 EVOTVLLKG 12

RESULT 2
CHEP_PARID STANDARD; PRT; 13 AA.

ID: CHEP_PARID
AC P42718;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Chemotactic peptide.
OS Parapolybia indica.

P17229 pisum sativ
P6535 canis famili
P80867 bacillus su
P82386 litoria ran
P82387 litoria ran
P1020 bothrops ja
P17237 icaria sp.
P17235 vespula lew
P28489 bos taurus
P31832 rana escula
P24963 homo sapien
P20525 hordeum vul

NEUT_CAVPO STANDARD; PRT; 13 AA.
 ID NEUT_CAVPO
 AC P32560;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotensin (NT).
 GN NTS.
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OC NCBI_TaxID:10141;
 RN [1]
 RP
 RC TISSUE=Small intestine;
 RX MEDLINE=8648085; PubMed=3087775;
 RA Shaw C., Thim L., Conlon J.M.;
 RT *"(Ser)neurotensin: isolation from guinea pig intestine."*;
 RL *FBBs Lett.* 202:187-192 (1986).
 CC -!- FUNCTION: Smooth muscle-contracting peptide.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the neurotensin family.
 DR PIR: A53608; A55608.
 KW Vasoactive; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1680 MW; 4C814644C4115B3 CRC64;
 Query Match 25.4%; Score 17; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 PYYL 10
 Db 10 PYYL 13

RESULT 7
NEUT_CHICK STANDARD; PRT; 13 AA.
 ID NEUT_CHICK
 AC P13724;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotensin (NT).
 OS *Gallus gallus* (Chicken).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP
 SEQUENCE.
 RX MEDLINE=8063566; PubMed=3682409;
 RA Iwabuchi R., Komori S., Ohashi H., Kimura S.;
 RT "The amino acid sequence of a smooth muscle-contracting peptide from
 chicken rectum. Identity to chicken neurotensin.";
 RL Jpn. J. Pharmacol. 44:455-459 (1987).
 CC -!- FUNCTION: Smooth muscle-contracting peptide.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the neurotensin family.
 DR PIR: A28505; A28505.
 KW Vasoactive; Pyrrolidone carboxylic acid.
 FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1608 MW; 4C9495714C410DD3 CRC64;
 Query Match 25.4%; Score 17; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 PYYL 10
 Db 10 PYYL 13

RESULT 8
NEUT_RANTE STANDARD; PRT; 13 AA.
 ID NEUT_RANTE
 AC P41536;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotensin (NT).
 OS *Rana temporaria* (European common frog).
 OC Rana; Rana temporaria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OC NCBI_TaxID:8407;
 RN [1]
 RP
 SEQUENCE.
 RX MEDLINE=92245104; PubMed=1574601;
 RA Shaw C., McKay D.M., Halton D.W., Thim L., Buchanan K.D.;
 RT *"Isolation and primary structure of an amphibian neurotensin."*;
 RL Regul. Pept. 38:23-31 (1992).
 CC -!- FUNCTION: Smooth muscle-contracting peptide.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Identified in brain, intestine, and rectum,
 but not in stomach or skin.
 CC -!- SIMILARITY: Belongs to the neurotensin family.
 DR PIR: A61067; A61067.
 KW Vasoactive; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1569 MW; 56A53D969EF410DD3 CRC64;
 Query Match 25.4%; Score 17; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 PYYL 10
 Db 10 PYYL 13

RESULT 9
TY13_PHYRO STANDARD; PRT; 13 AA.
 ID TY13_PHYRO
 AC P04055;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tryptophyllin-13.
 OS *Phylomedusa rohdei* (Rohde's leaf frog).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyliidae;
 OC Phylomedusine; Phylomedusa.
 OC NCBI_TaxID=8394;
 RN [1]
 RP
 SEQUENCE.
 RA Montecuccoli P.C., Gozzini L., Bresamer V.;
 RT "Primary structure determination of a tryptophan-containing
 tridecapeptide from *Phylomedusa rohdei*.";
 RL *Int. J. Pept. Protein Res.* 27:175-182 (1986).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR: A05174; A05174.
 KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A2122773 CRC64;
 Query Match 25.4%; Score 17; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 QVSPY 8
 Db 1 QEKPY 5

| | | | | | |
|--|-----------|------|----|--------|----|
| PEDI_HYDAT | ID | Db | 6 | YAVI0Q | 11 |
| PEDI_HYDAT | STANDARD; | PRT; | 13 | AA. | |
| AC P80578; | | | | | |
| DT 01-OCT-1996 (Rel. 34, Last sequence update) | | | | | |
| DT 01-OCT-1996 (Rel. 34, Last annotation update) | | | | | |
| DE pedin. | | | | | |
| OS Hydra attenuata (Hydra) (Hydra vulgaris). | | | | | |
| RT Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae; | | | | | |
| OC Hydridae; Hydra; | | | | | |
| OX NCBI_TAXID=6087; | | | | | |
| RN [1] | | | | | |
| RP SEQUENCE. | | | | | |
| RX MEDLINE=96232307; PubMed=8674432; | | | | | |
| RX Hoffmeister S.A.H. | | | | | |
| RT "Isolation and characterization of two new morphogenetically active peptides from Hydra vulgaris."; | | | | | |
| RT Development 122:1941-1948(1996). | | | | | |
| CC -!- FUNCTION: Morphogenetically active peptide. Active in foot development. | | | | | |
| KW Morphogen. | | | | | |
| SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64; | | | | | |
| Query Match 23.9%; Score 16; DB 1; Length 13; | | | | | |
| Best Local Similarity 37.5%; Pred. No. 5e+03; | | | | | |
| Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0; | | | | | |
| QY 3 EQVSPYTL 10 | | | | | |
| Db 1 EEDRPEVL 8 | | | | | |
| RESULT 11 | | | | | |
| PROX_ORYSA | STANDARD; | PRT; | 13 | AA. | |
| ID PROX_ORYSA | | | | | |
| AC P83647; | | | | | |
| DT 10-OCT-2003 (Rel. 42, Last sequence update) | | | | | |
| DT 10-OCT-2003 (Rel. 42, Last annotation update) | | | | | |
| DE Probable profilin LP04 (Fragments). | | | | | |
| OS Oryza sativa (Rice). | | | | | |
| OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. | | | | | |
| OC ERIBHAROIDEAE; ORYZEAE; ORYZA. | | | | | |
| OX NCBI_TAXID=4530; | | | | | |
| [1] | | | | | |
| RP SEQUENCE. | | | | | |
| RC Indica-IR64; TISSUE=Panicle; Hosseini Sajedeh S.G.; Bennett J.; "Proteome analysis of rice panicle."; | | | | | |
| RT Submitted (JUL-2003) to Swiss-Prot. | | | | | |
| CC -!- FUNCTION: Binds to actin and affects the structure of the cytoskeleton. At high concentrations, profilin prevents the polymerization of actin, whereas it enhances it at low concentrations. By binding to PIP2, it inhibits the formation of IP3 and DG (By similarity). | | | | | |
| CC -!- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric actin in a 1:1 ratio. | | | | | |
| CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is 4.4, its MW is: 14.0 kDa. | | | | | |
| CC -!- SIMILARITY: Belongs to the profilin family. | | | | | |
| CC DR PROSITE; PS0014; PROFILIN; PARTIAL. | | | | | |
| KW Actin-binding; Cytoskeleton; Multigene family. | | | | | |
| FT NON_TER 1 | | | | | |
| FT NON_CONS 5 | | | | | |
| FT NON_TER 13 | | | | | |
| SQ SEQUENCE 13 AA; 1362 MW; 0A3022EE0B52C68B CRC64; | | | | | |
| Query Match 23.9%; Score 16; DB 1; Length 13; | | | | | |
| Best Local Similarity 33.3%; Pred. No. 5e+03; | | | | | |
| Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0; | | | | | |
| QY 8 YTLIKG 13 | | | | | |

Db 4 VLRG 7

RESULT 14

ID ACT7_SOYBN STANDARD; PRT; 13 AA.

AC P15987; DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Actin-7 (Fragment)

GN SACT7.

OS Glycine max (Soybean).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Peleodryadinae; Litoria.

OC NCBI_TaxID:104895;

RN [1]

RP SEQUENCE.

RC TISSUE-Skin secretion;

RA Wabbitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;

RT "Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella.";

RT Aust. J. Chem. 52:639-645 (1999).

RL CC -!- SUBCELLULAR LOCATION: Secreted.

RX CC -!- TISSUE SPECIFICITY: Skin.

RA Pearson L., Meagher R.B.;

RT Diverse soybean actin transcripts contain a large intron in the 5' untranslated leader: structural similarity to vertebrate muscle actin genes. ;

RT RL Plant Mol. Biol. 14:513-526 (1990).

CC CC -- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.

CC CC -- FUNCTION: Essential component of cell cytoskeleton; plays an important role in cytoplasmic streaming, cell shape determination, cell division, organelle movement and extension growth.

CC CC --!- SUBCELLULAR LOCATION: Cyttoplasmic.

CC CC --!- MISCELLANEOUS: There are at least 16 actin genes in soybean.

CC CC --!- SIMILARITY: Belongs to the actin family.

CC CC

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CC CC

CC DR EMBL; X17120; CAA34380.1; -.

CC DR PIR; S15755; S15755.

CC DR InterPro; IPR004001; Actin.

CC DR InterPro; IPR004000; Actin-like.

CC DR PROSITE; PS00405; ACTINS_1; PARTIAL.

CC DR PROSITE; PS00422; ACTINS_2; PARTIAL.

CC DR PROSITE; PS0112; ACTINS_ACT_LIKE; PARTIAL.

CC DR KW structural protein; Multi-gene family.

FT FT NON_TER 13 13

SQ SEQUENCE 13 AA: 1420 MW: 8BEEFF3C36D4FD05A CRC64;

Query Match 22.4%; Score 15; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 7.8e+03; Pairs 2;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PQVSP 7

Dy 5 EDIQP 9

RESULT 15

ID E121_LITRU STANDARD; PRT; 13 AA.

AC P82057; DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Electrin 2.1.

OS Litoria rubella (Dessert tree frog).

Pathé
School

DT 01-JUN-2003 (TREMBrel. 24, last annotation update)
 DR CetE7 protein (Fragment).
 GN CetE7.
 OS Escherichia coli.
 OG Plasmid CetE7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 RN [1] NCBI_TaxID=562;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92293113; PubMed=1603061;
 RA "Song B.W., Lu F.M., Chak K.R.,
 Mol. Genet. 231:177-183(1992)."
 RL EMBL; M62409; AAA98055.1;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR InterPro; IPR000290; Colicin_pyocin.
 DR Pfam; PF01320; Colicin_pyocin; 1.
 FT NON_TER. 13 AA; 1501 MW; 9E75F892148CB045 CRC64;
 SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;
 Query Match 28.4%; Score 19; DB 2; Length 13;
 Best Local Similarity 37.5%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 QEQVSPY 9
 Db 4 KNSISDYT 11
 RESULT 3
 ORG00 PRELIMINARY; PRT; 13 AA.
 ID OGRG00
 AC OGRG00;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment);
 OS Mycoplasma capricolum subsp. capricolum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 RN [1] NCBI_TaxID=40479;
 RP SEQUENCE FROM N.A.
 RC STRAIN=8035;
 RX MEDLINE=2013983; PubMed=10727835;
 RA Thiaucourt F., Lorenzon S., David A., Bredard A.;
 RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
 of a putative membrane protein gene.";
 RL J. Microbiol. 72:250-268(2000).
 DR EMBL; AF11547.1; -.
 KW Hypothetical protein.
 FT NON_TER. 1 AA; 1459 MW; 0B6338AED35573B CRC64;
 SQ SEQUENCE 13 AA; 1531 MW; 93F7EB96FDBBCB1A CRC64;
 Query Match 28.4%; Score 19; DB 2; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 SPYMLIK 12
 Db 4 TPYLIKK 10
 RESULT 4
 ID Q14890
 AC Q14890;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE Mucin (Fragment).
 GN MUC5AC.

OS Homo sapiens (Human).
 OC Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE=Tracheobronchial mucosa;
 RA Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M.,
 RA Zouitina-Galiegue S., Pigny P., Degand P., Aubert J., Porchet N.;
 RT "Characterization of the human mucin gene MUC5AC: a consensus
 cysteine-rich domain for lipoprotein mucin genes.";
 RL Biochem. J. 0-0(1994).
 DR EMBL; Z34280; CAA84034.1; -.
 FT NON_TER. 1 AA; 13 MW; 1380 MW; 535DF5A5183B7767 CRC64;
 SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;
 Query Match 28.4%; Score 19; DB 4; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 NQEQVSP 7
 Db 2 NKGQLPP 8
 RESULT 5
 ID 048357
 AC 048357
 PRELIMINARY; PRT; 13 AA.
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DB Transcription termination factor rho (Fragment).
 GN RHO.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 RN NCBI_TaxID=562;
 [1] SEQUENCE FROM N.A.; PubMed=7828920;
 RX MEDLINE=95129907;
 RA Opperman T., Martinez A., Richardson J.P.;
 RT "The ts15 mutation of Escherichia coli alters the sequence of the C-
 terminal nine residues of Rho protein.";
 RL Gene 152:133-134(1995).
 DR EMBL; L34404; AA66985.1; -.
 FT NON_TER. 1 AA; 13 MW; 1531 MW; 93F7EB96FDBBCB1A CRC64;
 SQ SEQUENCE 13 AA; 1531 MW; 93F7EB96FDBBCB1A CRC64;
 Query Match 26.9%; Score 18; DB 2; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.8e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 NQEQVSP 7
 Db 5 NDEVMTP 11
 RESULT 6
 ID 050476
 AC 050476
 PRELIMINARY; PRT; 13 AA.
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE Catalase.
 GN KATG.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacteriinae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]

RP SEQUENCE FROM N.A.
 RC SPRINT=L10373;
 RA Cockerill F.R.; Uhl J.R.; Temesgen Z.; Zhang Y.; Stockman L.;
 RA Roberts G.D.; Williams D.L.; Kline B.C.;
 RT "Rapid Identification of a point mutation of the *Mycobacterium isoniazid*
 RT tuberculosis catalase-peroxidase (katG) gene associated with isoniazid
 resistance.";
 RT submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U06263; AAB59976.1; -;
 SEQUENCE 13 AA; 1564 MW; 2F39A45EFE94777 CRC64;

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 2.7e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQVSPYT 9
 Db 3 EQHSPIT 9

RESULT 7

ID 093824 PRELIMINARY; PRT; 13 AA.
 AC 093824; 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 ID 093824; 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DE UDP-galactose-4-epimerase (Fragment).
 GN GAL10.
 OS *Candida tropicalis* (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetidae; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; *Candida*.
 OC NEBI_TAXID=5482;
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=PK233;
 RT Karai T.; Ueda M.; Tanaka A.; *Candida tropicalis* promoter region of GAL1 and GAL10 gene. ";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB019434; BAA34351.1; -;
 FT NON-TER 1
 FT SEQUNCE 13 AA; 1312 MW; 0B559D6AB18BC720 CRC64;

Query Match 23.9%; Score 16; DB 3; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.2e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YTLVKG 13
 Db 5 YLVTG 10

RESULT 8

ID Q9PSA8 PRELIMINARY; PRT; 13 AA.
 AC Q9PSA8; 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE RNA polymerase II (Fragment).
 RN RPB2.

Q9PSA8 Silene baccifera (Berry catchfly) (*Cucubalus baccifer*).
 OS Silene baccifera (Berry catchfly); Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene. NCBI_TAXID=54818;
 RN [1]

SEQUENCE FROM N.A.

RP S9PSA8 PRELIMINARY; PRT; 13 AA.
 AC S9PSA8; 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE RNA polymerase II (Fragment).
 RN RPB2.

Q9PSA8 Silene pentelica. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene. NCBI_TAXID=49735;
 RN [1]

SEQUENCE FROM N.A.

RP P0PP M.; Oxelman B.; 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 RT "Inferreding the history of the polyploid *Silene aegaea* (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RT submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AU296132; CAC13024.1; -;
 FT NON-TER 1
 FT NON-TER 13 13 13 MW; D931E2C1AB6D1B2 CRC64;

Query Match 23.9%; Score 16; DB 10; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.2e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPYT 9
 Db 1 TPFT 4

RESULT 9

ID Q98NL1 PRELIMINARY; PRT; 13 AA.
 AC Q98NL1; 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Calmodulin (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OC NEBI_TAXID=4513; [1]

SEQUENCE FROM N.A.

RP MEDLINE:94266769; PubMed=8206888;
 RA Toda H.; Yazawa M.; Sakiyama F.; Yagi K.;
 RT "Amino acid sequence of calmodulin from wheat germ.";
 RL J. Biochem. 115:367-367(1994).
 SEQUENCE 13 AA; 1508 MW; 9763F31CD443DB1A CRC64;

Query Match 23.9%; Score 16; DB 10; Length 13;
 Best Local Similarity 33.3%; Pred. No. 4.2e+04;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQVSPYT 8
 Db 7 EQIAEF 12

RESULT 10

ID Q9PS94 PRELIMINARY; PRT; 13 AA.
 AC Q9PS94; 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE RNA polymerase II (Fragment).
 RN RPB2.

Q9PS94 Silene pentelica. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene. NCBI_TAXID=49735;
 RN [1]

SEQUENCE FROM N.A.

RP P0PP M.; Oxelman B.; 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 RT "Inferreding the history of the polyploid *Silene aegaea* (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
 RT submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AU296132; CAC13024.1; -;
 FT NON-TER 1
 FT NON-TER 13 13 13 MW; D931E2C1AB6D1B2 CRC64;

Query Match 23.9%; Score 16; DB 10; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.2e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPYT 9
 Db 1 TPFT 4

| | | | |
|---|-----|-----------|--|
| QY | 6 | SPYPT 9 | RESULT 13 |
| | : : | | Q9W45 |
| Db | 1 | TPFT 4 | PRELIMINARY; PRT; 13 AA. |
| RESULT 11 | | | |
| Q47693 | | | ID Q9W45 |
| AC Q47693; | | | PRELIMINARY; PRT; 13 AA. |
| DT 01-NOV-1996 | | | ID Q9W45; |
| (TREMBrel. 01, Created) | | | AC Q9W45; |
| DT 01-NOV-1996 | | | DT 01-MAY-2000 (TREMBrel. 13, Last sequence update) |
| (TREMBrel. 01, Last sequence update) | | | DT 01-MAY-2000 (TREMBrel. 21, Last annotation update) |
| DT 01-JUN-2003 | | | DE GTP-binding protein RAB16 (Fragment). |
| (TREMBrel. 24, Last annotation update) | | | OS Rattus sp. |
| DE Elongation factor TU (EF-TU) (Fragment). | | | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |
| GN TUF. | | | OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |
| OS Bacteriia; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. | | | OX NCBI_TaxID=62; |
| OC | | | OX NCBI_TaxID=62; |
| OX NCBI_TaxID=62; | | | RN [1] |
| RN | | | SEQUENCE FROM N.A. |
| RP SEQUENCE FROM N.A. | | | RX MEDLINE:82080657; PubMed=7312036; |
| RX MEDLINE:82080657; | | | RA Elferink L.A., Anzai K., Scheller R.H.; |
| RA Hudson L., Rosi J., Landy A.; | | | RT "rab15, a novel low molecular weight GTP-binding protein specifically expressed in rat brain."; |
| RT "Dual function transcripts specifying tRNA and mRNA. "; | | | RL J. Biol. Chem. 267:22693-22693(1992). |
| RL Nature 294:422-427(1981). | | | FT NON_TER 1 |
| DR EMBL: X04181; CAM2777.1; -; | | | FT NON_TER 13 |
| DR GO:000346; Translation elongation factor activity; IEA. | | | SQ SEQUENCE 13 AA; 1584 MW; 40BD5FE7236041A3 CRC64; |
| DR GO: GO:0006412; Protein biosynthesis; IEA. | | | Query Match 22.4%; Score 15; DB 11; Length 13; |
| KW Elongation factor; Protein biosynthesis. | | | Best local Similarity 33.3%; Pred. No. 6.5e+04; Mismatches 2; Indels 0; Gaps 0; |
| FT NON_TER 13 AA; 1617 MW; C433BE82A18D0819 CRC64; | | | DB 7 ERTPH 12 |
| SQ SEQUENCE 13 AA; 1617 MW; 0B79431F5635573B CRC64; | | | Query Match 22.4%; Score 15; DB 11; Length 13; |
| RESULT 12 | | | Best local Similarity 33.3%; Pred. No. 6.5e+04; Mismatches 2; Indels 0; Gaps 0; |
| Q9FZ4 | | | DB 3 EQVSPY 8 |
| AC Q9FZ4; | | | Query Match 22.4%; Score 15; DB 11; Length 13; |
| DT 01-MAY-2000 | | | Best local Similarity 33.3%; Pred. No. 6.5e+04; Mismatches 2; Indels 0; Gaps 0; |
| (TREMBrel. 13, Last sequence update) | | | DB 7 ERTPH 12 |
| QY | 3 | EQVSPY 8 | DB 4 QVSPY 9 |
| | : : | | DB 4 QVSPY 9 |
| Db | 7 | ERTKPH 12 | Db 4 QVSPY 9 |
| RESULT 12 | | | Db 4 QVSPY 9 |
| Q9FZ4 | | | Db 4 QVSPY 9 |
| AC Q9FZ4; | | | RESULT 14 |
| DT 01-MAY-2000 | | | ID Q9QY46 |
| (TREMBrel. 13, Last sequence update) | | | PRELIMINARY; PRT; 13 AA. |
| QY | 3 | ERTKPH 12 | ID Q9QY46; |
| | : : | | AC Q9QY46; |
| Db | 7 | | DT 01-MAY-2000 (TREMBrel. 13, Last sequence update) |
| RESULT 12 | | | DT 01-MAY-2000 (TREMBrel. 13, Last annotation update) |
| Q9FZ4 | | | DB Zfp127 protein (Fragment). |
| AC Q9FZ4; | | | OS Mus sp. |
| DT 01-MAY-2000 | | | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| (TREMBrel. 13, Last sequence update) | | | OC NCBI_TaxID=1095; |
| QY | 3 | ERTKPH 12 | RN [1] |
| | : : | | SEQUENCE FROM N.A. |
| Db | 7 | | RX MEDLINE:2-005261A; PubMed=10588722; |
| RESULT 12 | | | RA Greatly J.M., Gray T.A., Gabriel J.M., Song L., Zemel S., Nicholls R.D., |
| Q9FZ4 | | | RT "Conserved characteristics of heterochromatin-forming DNA at the 15q11-q13 imprinting center," |
| AC Q9FZ4; | | | RT 15q11-q13 imprinting center," |
| DT 01-OCT-2003 | | | RL Proc. Natl. Acad. Sci. U.S.A. 96:14430-14435(1999). |
| (TREMBrel. 25, Last annotation update) | | | DR EMBL: A130348; ADP56756.1; -; |
| DE Hypothetical protein (Fragment). | | | FT NON_TER 13 |
| OS Mycoplasma mycooides subsp. capri. | | | SQ SEQUENCE 13 AA; 1356 MW; D89F5BA9529476D CRC64; |
| OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma. | | | Query Match 22.4%; Score 15; DB 11; Length 13; |
| OX NCBI_TaxID=40477; | | | Best local Similarity 33.3%; Pred. No. 6.5e+04; Mismatches 2; Indels 0; Gaps 0; |
| RN [1] | | | DB 7 ERTPH 12 |
| RP SEQUENCE FROM N.A. | | | Query Match 22.4%; Score 15; DB 11; Length 13; |
| RC STRAIN=PO3; | | | Best local Similarity 33.3%; Pred. No. 6.5e+04; Mismatches 2; Indels 0; Gaps 0; |
| RX MEDLINE:20193983; PubMed=10727835; | | | DB 7 ERTPH 12 |
| RA Thiaucourt F., Lorenzen S., Breard A.; | | | Query Match 22.4%; Score 15; DB 11; Length 13; |
| RT "Phylogeny of the Mycoplasma mycooides cluster as shown by sequencing of a putative membrane protein gene."; | | | Best local Similarity 33.3%; Pred. No. 6.5e+04; Mismatches 2; Indels 0; Gaps 0; |
| RT of a putative membrane protein gene."; | | | DB 7 ERTPH 12 |
| RL Vert. Microbiol. 72:251-268(2000). | | | Query Match 22.4%; Score 15; DB 11; Length 13; |
| DR EMBL: A162989; AAF15253.1; -. | | | Best local Similarity 33.3%; Pred. No. 6.5e+04; Mismatches 2; Indels 0; Gaps 0; |
| KW Hypothetical protein. | | | DB 7 ERTPH 12 |
| FT NON_TER 13 AA; 1505 MW; 0B79431F5635573B CRC64; | | | Query Match 22.4%; Score 15; DB 11; Length 13; |
| SQ SEQUENCE 13 AA; 1505 MW; 0B79431F5635573B CRC64; | | | Best local Similarity 33.3%; Pred. No. 6.5e+04; Mismatches 2; Indels 0; Gaps 0; |
| RESULT 15 | | | DB 7 ERTPH 12 |
| QY | 7 | PYT1 10 | RN 088176 |
| | : : | | PRELIMINARY; PRT; 13 AA. |
| Db | 5 | PYL1 8 | ID 088176; |
| RESULT 15 | | | AC 088176; |
| QY | 7 | PYT1 10 | DT 01-NOV-1998 (TREMBrel. 08, Created) |
| | : : | | DT 01-NOV-1998 (TREMBrel. 08, Last sequence update) |
| Db | 5 | PYL1 8 | DT 01-OCT-2002 (TREMBrel. 22, Last annotation update) |
| RESULT 15 | | | DB Neural cell adhesion molecule (Fragment). |

GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb-C; TISSUE=Liver;
 RX MEDLINE=98250618; PubMed=9562442;
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
 RT "A cis-acting regulatory element that affects the alternative splicing
 of a muscle-specific exon in the mouse NCAM gene.";
 RL Bicchim, Biophys. Acta 1397:305-315(1998).
 DR EMBL; ABC01873; BAA31275.1; -.
 DR MGD; MGI:97281; Ncam1.
 FT NON-TER 1 1
 FT 13 13
 FT SEQUENCE 13 AA; 1495 MW; CC6098E54C72D732 CRC64;
 SQ

Query Match 22.4%; Score 15; DB 11; Length 13;
 Best Local Similarity 42.9%; Pred. No. 6.5e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Caps 0;
 Ov 5 VSPYTL 11
 Db 7 LOPQCL 13

Search completed: October 1, 2004, 13:50:08
 Job time : 39 secs

Frank

Spicer

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: October 1, 2004, 13:48:03 ; Search time 17 Seconds

(without alignments)
3.9.479 Million cell updates/sec

Title: US-09-674-616A-2
Perfect score: 67
Sequence: 1 NOEQVSPYTLKG 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 6327

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/protdata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/protdata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/protdata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/protdata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/protdata/2/iaa/PCUTS_COMB.pep: *
6: /cgn2_6/protdata/2/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|--------------------|
| 1 | 36 | 53.7 | 13 | 4 | US-09-675-922-1 |
| 2 | 24 | 35.8 | 13 | 1 | US-09-174-477-6 |
| 3 | 24 | 35.8 | 13 | 3 | US-08-152-011-6 |
| 4 | 23 | 34.3 | 13 | 2 | US-08-620-213-3 |
| 5 | 23 | 34.3 | 13 | 2 | US-08-542-666-1 |
| 6 | 23 | 34.3 | 13 | 2 | US-08-332-522A-69 |
| 7 | 22 | 32.8 | 13 | 1 | US-08-068-947-14 |
| 8 | 22 | 32.8 | 13 | 1 | US-08-068-947-15 |
| 9 | 22 | 32.8 | 13 | 3 | US-08-750-419A-22 |
| 10 | 22 | 32.8 | 13 | 4 | US-09-468-588-11 |
| 11 | 22 | 32.8 | 13 | 4 | US-09-868-839-11 |
| 12 | 22 | 32.8 | 13 | 4 | US-09-811-672-19 |
| 13 | 21 | 31.3 | 13 | 1 | US-08-068-947-19 |
| 14 | 20.5 | 30.6 | 13 | 3 | US-09-040-116-8 |
| 15 | 20 | 29.9 | 13 | 1 | US-08-068-947-21 |
| 16 | 20 | 29.9 | 13 | 3 | US-08-630-916A-6 |
| 17 | 20 | 29.9 | 13 | 3 | US-08-630-916A-85 |
| 18 | 20 | 29.9 | 13 | 4 | US-08-630-915A-142 |
| 19 | 20 | 29.9 | 13 | 4 | US-09-297-369A-7 |
| 20 | 20 | 29.9 | 13 | 4 | US-09-635-872A-52 |
| 21 | 20 | 29.9 | 13 | 4 | US-09-636-077A-52 |
| 22 | 20 | 29.9 | 13 | 4 | US-09-543-608A-29 |
| 23 | 20 | 29.9 | 13 | 4 | US-09-543-608A-30 |
| 24 | 20 | 29.9 | 13 | 4 | US-09-543-608A-31 |
| 25 | 20 | 29.9 | 13 | 4 | US-09-636-060C-52 |
| 26 | 20 | 29.9 | 13 | 4 | US-09-986-552-52 |
| 27 | 19 | 28.4 | 13 | 4 | US-08-068-947-8 |
| 28 | 19 | 28.4 | 13 | 1 | US-09-068-947-24 |
| 29 | 19 | 28.4 | 13 | 1 | US-08-465-005A-13 |
| 30 | 19 | 28.4 | 13 | 1 | US-08-471-033-11 |
| 31 | 19 | 28.4 | 13 | 1 | US-08-471-044-11 |
| 32 | 19 | 28.4 | 13 | 2 | US-08-471-044-11 |
| 33 | 19 | 28.4 | 13 | 2 | US-08-471-044-11 |
| 34 | 19 | 28.4 | 13 | 2 | US-08-465-009-7 |
| 35 | 19 | 28.4 | 13 | 2 | US-08-471-046A-11 |
| 36 | 19 | 28.4 | 13 | 2 | US-08-470-566B-11 |
| 37 | 19 | 28.4 | 13 | 2 | US-08-469-007-7 |
| 38 | 19 | 28.4 | 13 | 2 | US-08-838-219B-11 |
| 39 | 19 | 28.4 | 13 | 2 | US-08-439-334-11 |
| 40 | 19 | 28.4 | 13 | 3 | US-08-630-916A-58 |
| 41 | 19 | 28.4 | 13 | 3 | US-08-831-094-42 |
| 42 | 19 | 28.4 | 13 | 3 | US-09-309-529-11 |
| 43 | 19 | 28.4 | 13 | 3 | US-09-233-338A-11 |
| 44 | 19 | 28.4 | 13 | 3 | US-09-233-752A-11 |
| 45 | 19 | 28.4 | 13 | 3 | US-09-024-557-5 |

ALIGNMENTS

RESULT 1
US-09-675-922-1
; Sequence 1, Application US/09675922
; Patent No. 648731
; GENERAL INFORMATION:
; APPLICANT: Hubbell A., Jeffrey
; APPLICANT: Schense C., Jason
; APPLICANT: Sakiyama E., Shelley
; TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue
; TITLE OF INVENTION: Engineering: Incorporation of Proteins
; FILE REFERENCE: EPO 107 DIV
; CURRENT APPLICATION NUMBER: US/09/675, 922
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Factor XIIa at
; OTHER INFORMATION: N-terminal and modified peptide from the
; OTHER INFORMATION: heparin-binding domain of ATII
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: dansyl leucine
; US-09-675, 922-1
; Query Match % 53.7%; Score 36; DB 4; Length 13;
; Best Local Similarity 100.0%; Pred. No. 1.3;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 NOEQVSP 7
; DB 2 NOEQVSP 8

RESULT 2
US-08-174-467-6
; Sequence 6, Application US/08174467
; Patent No. 5451514
; GENERAL INFORMATION:
; APPLICANT: BOUDET, ALAIN M.
; APPLICANT: INZE, DIRK G.
; APPLICANT: SCHUCH, WOLFGANG W.
; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/174,467
 FILING DATE: 28-DEC-1993
 CLASSIFICATION: 300

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/874,166
 FILING DATE: 27-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-174-467-6

Query Match 35.8%; Score 24; DB 1; Length 13;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VSPYT 9 :|||
 Db 5 LSPYT 9

RESULT 3
 US-08-152-071-6

Sequence 6, Application US/08452071
 Patent No. 6065780

GENERAL INFORMATION:
 APPLICANT: BOUDET, ALAIN M.
 APPLICANT: INZ, DIRK G.
 APPLICANT: SCHUCH, WOLFGANG W.

TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN PLANTS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eversen, McKeown, Edwards & Lenahan
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/620,213
 FILING DATE:
 CLASSIFICATION: 544

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 195 10 566,4
 FILING DATE: 23-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D.
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 181/42626

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-620-213-3

Query Match 35.8%; Score 24; DB 3; Length 13;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VSPYT 9 :|||
 Db 5 LSPYT 9

RESULT 4
 US-08-620-213-3

Sequence 3, Application US/08620213
 Patent No. 5677297

GENERAL INFORMATION:
 APPLICANT: WALDECK, Harald
 APPLICANT: HOELZLE, Dagmar
 APPLICANT: MESSINGER, Josef
 APPLICANT: ANTEL, Jochen
 APPLICANT: THORMAELLEN, Dirk
 APPLICANT: WURL, Michael

TITLE OF INVENTION: BENZAZEPINE-, BENZOKAZEPINE- AND BENZOTIAZEPINE-N-ACETIC ACID DERIVATIVES, PROCESS FOR THEIR PREPARATION AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM

TITLE OF INVENTION: BENZAZEPINE-, BENZOKAZEPINE- AND BENZOTIAZEPINE-N-ACETIC ACID DERIVATIVES, PROCESS FOR THEIR PREPARATION AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eversen, McKeown, Edwards & Lenahan
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/620,213
 FILING DATE:
 CLASSIFICATION: 544

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 195 10 566,4
 FILING DATE: 23-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D.
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 181/42626

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-620-213-3

Query Match 34.3%; Score 23; DB 1; Length 13;
 Best Local Similarity 62.5%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 10
 Db 5 EHVVVYGL 12

RESULT 5
 US-08-542-686-1
 Sequence 1, Application US/08542686
 Patent No. 582487

GENERAL INFORMATION:
 APPLICANT: Ravetch, Jeffrey V.
 COMPUTER: Kuroakki, Tomoniro
 TITLE OF INVENTION: METHOD FOR SCREENING FOR TARGETS FOR
 NUMBER OF SEQUENCES: 9
 NUMBER OF SEQUENCES: 136
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112

MEDIUM READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/542,686
 FILING DATE: 23-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John J.
 REGISTRATION NUMBER: 28,678
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/052,269
 FILING DATE: 23-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John J.
 REGISTRATION NUMBER: 28,678
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 42113/JPW/AKC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEX: (212) 664-0525
 TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-332-562A-69

Query Match 34.3%; Score 23; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 12
 Db 1 ENRTYSLIK 10

RESULT 7
 US-08-068-947-14
 Sequence 14, Application US/08068947
 Patent No. 5470753

GENERAL INFORMATION:
 APPLICANT: Sepekov, Nikolai
 APPLICANT: Lissakova, Olga
 APPLICANT: Krchnak, Viktor
 APPLICANT: Lebl, Michal
 TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

Query Match 34.3%; Score 23; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 12
 Db 2 ENRTYSLIK 11

RESULT 6
 US-08-332-562A-69
 Sequence 69, Application US/08332562A
 Patent No. 5955599

GENERAL INFORMATION:
 APPLICANT: MCKENZIE, Ian F.C.

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/068,947
 FILING DATE: 19930528
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, Esq., S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7156-040-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864/9741
 MOLECULE TYPE: peptide
 TOPOLOGY: unknown
 LENGTH: 13 amino acids
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide
 QUERY MATCHES: 32.8%; Score: 22; DB: 1; Length: 13;
 BEST LOCAL SIMILARITY: 50.0%; Pred. No. 6.7e+02;
 PRED. NO.: 6.7e+02;
 MISMATCHES: 1; INDELS: 0; GAPS: 0;
 INDELS: 0;
 GAPS: 0;
 QY 2 QEQVSP 7
 DB 2 QDQIQP 7
 RESULT 9
 US-08-750-419A-22
 ; Sequence 22, Application US/08750419A
 ; Patent No. 6008340
 ; GENERAL INFORMATION:
 ; APPLICANT: BAILI, TANJA
 ; APPLICANT: VITALIA, SUSANNE
 ; APPLICANT: SPRR, WOLFGANG
 ; APPLICANT: VALENT, PETER
 ; APPLICANT: SUSSAN, MARKUS
 ; APPLICANT: KRAFT, DIETRICH
 ; APPLICANT: LAFER, SYLVIA
 ; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, RECOMBINANT RECOMBINANT DNA MOLECULES, VECTORS AND HOSTS
 ; TITLE OF INVENTION: CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC
 ; TITLE OF INVENTION: USES OF SAID ALLERGENS AND FRAGMENTS
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
 ; STREET: PO BOX 747
 ; CITY: FALLS CHURCH
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/750,419A
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1614-175
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-750-419A-22
 Query Match 32.8%; Score: 22; DB: 3; Length: 13;
 Best Local Similarity 50.0%; Pred. No. 6.7e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 EQQVSP 8
 DB 1 EPIAPY 6
 RESULT 10
 US-09-468-578-11

Sequence 11 Application US/09468578
 PATENT NO. 6399329
 GENERAL INFORMATION:
 APPLICANT: Wang, Huaming
 APPLICANT: Bodie, Elizabeth A.
 TITLE OF INVENTION: Phenol Oxidizing Enzymes
 FILE REFERENCE: GC561-3
 CURRENT APPLICATION NUMBER: US/09/468,578
 CURRENT FILING DATE: 1999-12-21
 PRIOR APPLICATION NUMBER: US 09/220,871
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: US 09/338,723
 PRIOR FILING DATE: 1999-06-23
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 13
 TYPE: PRT
 ORGANISM: *Stachybotrys chartarum*
 US-09-468-578-11
 RESULT 11
 Query Match 32.8%; Score 22; DB 4; Length 13;
 Best Local Similarity 80.0%; Pred. No. 6.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QVSPY 8
 Db 3 QVMPY 7
 US-09-866-839-11
 Sequence 11 Application US/09868839
 Patent No. 6509307
 GENERAL INFORMATION:
 APPLICANT: UNILEVER N.V. et al.
 TITLE OF INVENTION: DETERGENT COMPOSITIONS COMPRISING PHENOL OXIDIZING
 TITLE OF INVENTION: ENZYMES
 FILE REFERENCE: C7516 (V)
 CURRENT APPLICATION NUMBER: US/09/868,839
 PRIOR APPLICATION NUMBER: US 09/220,871
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: US 09/338,723
 PRIOR FILING DATE: 1999-06-23
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 13
 TYPE: PRT
 ORGANISM: *Stachybotrys chartarum*
 US-09-866-839-11
 Query Match 32.8%; Score 22; DB 4; Length 13;
 Best Local Similarity 80.0%; Pred. No. 6.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QVSPY 8
 Db 3 QVMPY 7
 US-09-866-839-11
 RESULT 12
 Query Match 31.3%; Score 21; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 2;
 APPLICANT: Balli, Tanja
 APPLICANT: Vrtala, Susanne
 APPLICANT: Sperr, Wolfgang
 APPLICANT: Valente, Peter
 APPLICANT: Susani, Markus
 APPLICANT: Kraft, Dietrich
 APPLICANT: Balli, Tanja
 APPLICANT: Vrtala, Susanne
 APPLICANT: Sperr, Wolfgang
 APPLICANT: Valente, Peter
 APPLICANT: Susani, Markus
 APPLICANT: Kraft, Dietrich
 Sequence 19 Application US/09811672
 Patent No. 6559120
 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrock Esq., S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 71156-040-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-849-9090
 TELEFAX: 212-849-8864/9741
 TELEX: 66141 PRINN
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-068-947-19
 Sequence 19 Application US/08068947
 Patent No. 5470753
 GENERAL INFORMATION:
 APPLICANT: Sepetov, Nikolai
 APPLICANT: Iissakova, Olga
 APPLICANT: Kichnak, Viktor
 APPLICANT: Lebl, Michal
 TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
 TITLE OF INVENTION: SPECTROMETRY
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penne & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10035
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: SYSTEM, Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/068,947
 FILING DATE: 19930528
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrock Esq., S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 71156-040-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-849-9090
 TELEFAX: 212-849-8864/9741
 TELEX: 66141 PRINN
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-068-947-19

QY 1 NOEQVSP 7
 : :
 Db 1 NEQQIQP 7

RESULT 14
 US-09-040-216-8
 ; Sequence 8, Application US/09040216
 ; Patent No. 6030942
 ; GENERAL INFORMATION:
 ; APPLICANT: COOPERMAN, ET AL., BARRY
 ; TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS, AND OTHER
 ; TITLE OF INVENTION: SMALL MOLECULES USEFUL FOR INHIBITING THE ACTIVITY OF
 ; FILE REFERENCE: 9594-63U1
 ; CURRENT APPLICATION NUMBER: US/09/040, 216
 ; CURRENT FILING DATE: 1998-03-17
 ; EARLIER APPLICATION NUMBER: 08/919, 748
 ; EARLIER FILING DATE: 1997-08-28
 ; EARLIER APPLICATION NUMBER: 60/025, 146
 ; EARLIER FILING DATE: 1996-08-30
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; FEATURE:
 ; OTHER INFORMATION: alpha 13 helix region of E. coli R1
 US-09-040-216-8

RESULT 15
 US-08-068-947-21
 ; Sequence 21, Application US/08068947
 ; Patent No. 5470753
 ; GENERAL INFORMATION:
 ; APPLICANT: Sepetov, Nikolai
 ; APPLICANT: Krchnak, Viktor
 ; APPLICANT: Lebl, Michal
 ; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
 ; TITLE OF INVENTION: SPECTROMETRY
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/068, 947
 FILING DATE: 1993-05-28
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock Esq., S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7156-040-999

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8964/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-068-947-21:
 Query Match 29.9%; Score 20; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.6e+03; 2; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 QVSPY 8
 : :
 Db 9 QVIPF 13

Search completed: October 1, 2004, 13:50:30
 Job time: 18 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 13:46:59 ; search time 45 seconds

Scoring table: BLOSUM62

Scoring: 92.964 Million cell updates/sec

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Maximum Match 100%
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34: /cgn2_6/prodata/2/pbpaal/US12C_PUBCOMB.pep:*

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36: /cgn2_6/prodata/2/pbpaal/US13_PUBCOMB.pep:*

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40: /cgn2_6/prodata/2/pbpaal/US14_PUBCOMB.pep:*

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42: /cgn2_6/prodata/2/pbpaal/US14C_PUBCOMB.pep:*

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45: /cgn2_6/prodata/2/pbpaal/US15A_PUBCOMB.pep:*

RESULT 1

US-10-323-046-22

Sequence 22, Application US/10323046

GENERAL INFORMATION:

APPLICANT: Hibbell, Jeffrey A

APPLICANT: Schenese, Jason C

APPLICANT: Sakiyama-Elbert, Shelly E

TIME OF INVENTION: Growth Factor Modified Protein Matrices for Tissue

TIME OF INVENTION: Engineering

FILE REFERENCE: ETH 107 CIP (2)

CURRENT APPLICATION NUMBER: US/10/323, 046

CURRENT FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: 09/141, 153

PRIOR FILING DATE: 1998-08-27

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 3.1

SEQ ID NO 22

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Peptide

FEATURE: NAME/KEY: MOD_RES

LOCATION: (1)

OTHER INFORMATION: damnsyl Leucine

US-10-323-046-22

Query Match 53.7%; Score 36; DB 14; Length 13;

Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NQEQQVSP 7

Db 2 NQEQQVSP 8

RESULT 2
 US-09-932-613-156
 ; Sequence 156, Application US/09932613
 ; Publication No. US20030091565A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; APPLICANT: Belitzer, James P.
 ; APPLICANT: Potter, M. Daniel
 ; APPLICANT: Fleming, Tony J.
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 ; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
 ; CURRENT APPLICATION NUMBER: US/09/932,613
 ; CURRENT FILING DATE: 2001-08-17
 ; NUMBER OF SEQ ID NOS: 458
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 156
 ; LENGTH: 13
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: BLYS binding polypeptide
 ; US-09-932-613-156
 ; Query Match, 35.8%; Score 24; DB 10; Length 13;
 ; Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 ; Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 QVSPTVLLK 12
 Db 2 QVDPETGILK 10

RESULT 3
 US-09-932-322-156
 ; Sequence 156, Application US/09932322
 ; Publication No. US20030194743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DyaX Corp.
 ; APPLICANT: Belitzer, James P.
 ; APPLICANT: Potter, M. Daniel
 ; APPLICANT: Fleming, Tony J.
 ; APPLICANT: Lasher, Robert Charles
 ; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)
 ; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
 ; CURRENT APPLICATION NUMBER: US/09/932,322
 ; CURRENT FILING DATE: 2001-08-17
 ; NUMBER OF SEQ ID NOS: 458
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 156
 ; LENGTH: 13
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: BLYS binding polypeptide
 ; US-09-932-322-156

Query Match, 35.8%; Score 24; DB 10; Length 13;
 Best Local Similarity 65.7%; Pred. No. 1.3e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 QVSPTVLLK 12
 Db 2 QVDPETGILK 10

RESULT 4
 US-10-351-208-64
 ; Sequence 64, Application US/10361208
 ; Publication No. US2004009167A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rider, Todd H.
 ; TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS
 ; FILE REFERENCE: 0050-2041-003
 ; CURRENT APPLICATION NUMBER: US/10/1361,208
 ; PRIOR APPLICATION NUMBER: US 60/355,359
 ; PRIOR FILING DATE: 2002-02-07
 ; PRIOR APPLICATION NUMBER: US 60/355,022
 ; PRIOR FILING DATE: 2002-02-07
 ; CURRENT APPLICATION NUMBER: US 60/432,386
 ; PRIOR FILING DATE: 2002-12-10
 ; NUMBER OF SEQ ID NOS: 473
 ; SOFTWARE: FastSBQ for Windows Version 4.0
 ; SEQ ID NO 197
 ; LENGTH: 13
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: partial Hdj-1 sequence
 ; NAME/KEY: NON_CONS
 ; LOCATION: 7-8
 ; US-10-361-208-64

Query Match, 35.8%; Score 24; DB 15; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QEQVSP 7
 Db 7 QEQVLP 12

RESULT 5
 US-10-361-208-197
 ; Sequence 197, Application US/10361208
 ; Publication No. US2004009167A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rider, Todd H.
 ; TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS
 ; FILE REFERENCE: 0050-2041-003
 ; CURRENT APPLICATION NUMBER: US/10/1361,208
 ; PRIOR APPLICATION NUMBER: US 60/355,359
 ; PRIOR FILING DATE: 2002-02-07
 ; PRIOR APPLICATION NUMBER: US 60/355,022
 ; PRIOR FILING DATE: 2002-02-07
 ; CURRENT APPLICATION NUMBER: US 60/432,386
 ; PRIOR FILING DATE: 2002-12-10
 ; NUMBER OF SEQ ID NOS: 473
 ; SOFTWARE: FastSBQ for Windows Version 4.0
 ; SEQ ID NO 197
 ; LENGTH: 13
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: partial Hdj-1 sequence
 ; NAME/KEY: NON_CONS
 ; LOCATION: 7-8
 ; US-10-361-208-197

Query Match, 35.8%; Score 24; DB 15; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QEQVSP 7
 Db 7 QEQVLP 12

RESULT 6
 US-10-225-007-782
 ; Sequence 782, Application US/10226007
 ; Publication No. US20030105277A1

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; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 805
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
; US-10-226-007-782

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03; Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 NOEQVSPY 8
          :|:|||:|
Db 1 NEEPPPPY 8

RESULT 7
US-10-226-007-794
; Sequence 794, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 815
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
; US-10-226-007-794

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03; Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 NOEQVSPY 8
          :|:|||:|
Db 1 NEEPPPPY 8

RESULT 8
US-10-226-007-805
; Sequence 805, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 824
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
; US-10-226-007-824

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03; Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 NOEQVSPY 8
          :|:|||:|
Db 1 NEEPPPPY 9

RESULT 9
US-10-226-007-815
; Sequence 815, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/10226007
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 815
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
; US-10-226-007-815

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03; Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 NOEQVSPY 8
          :|:|||:|
Db 1 NEEPPPPY 11

```

Query Match 34.3%; Score 23; DB 14; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2e+03; 4; Mismatches保守性; Indels 1; Gaps 0; Matches 0;

QY 1 NOEQVSPY 8
 Db 5 NEERPPPPY 12

RESULT 11
 US-10-226-007-832
 Sequence 832, Application US/10226007
 Publication No. US2003010527A1
 GENERAL INFORMATION:
 APPLICANT: Myriad Genetics, Inc.
 APPLICANT: Morham, Scott
 APPLICANT: Zavitz, Kenton
 APPLICANT: Hobden, Adrian
 TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
 FILE REFERENCE: 5005.01
 CURRENT APPLICATION NUMBER: US/10/226,007
 CURRENT FILING DATE: 2002-11-15
 PRIOR APPLICATION NUMBER: US 60/313,883
 PRIOR FILING DATE: 2001-08-21
 NUMBER OF SEQ ID NOS: 1673
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 832
 LENGTH: 13
 TYPE: PRT
 ; ORGANISM: Human herpesvirus 4
 ; US-10-226-007-832

Query Match 34.3%; Score 23; DB 14; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2e+03; 4; Mismatches 1; Indels 0; Gaps 0; Matches 0;

QY 1 NOEQVSPY 8
 Db 6 NEERPPPPY 13

RESULT 12
 US-10-412-897-20
 Sequence 20, Application US/10412897
 Publication No. US2003022024A1
 GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
 TITLE OF INVENTION: POLYPEPTIDE, BMSK1-0020/0021
 FILE REFERENCE: D0193 NP
 CURRENT APPLICATION NUMBER: US/10/412,897
 CURRENT FILING DATE: 2003-04-11
 PRIOR APPLICATION NUMBER: U.S. 60/372,745
 PRIOR FILING DATE: 2002-04-12
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 20
 LENGTH: 13
 TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-412-897-20

Query Match 34.3%; Score 23; DB 15; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2e+03; 5; Mismatches 0; Indels 0; Gaps 0; Matches 0;

QY 2 QEQVSPY 6
 Db 2 QEQVSPY 6

RESULT 13
 US-10-412-897-20

Query Match 32.8%; Score 22; DB 9; Length 13;
 Best Local Similarity 50.0%; Pred. No. 3.2e+03; 3; Mismatches 1; Indels 0; Gaps 0; Matches 0;

QY 3 EQVSPY 8
 Db 1 EPIAPY 6

RESULT 14
 US-09-811-672-19
 Sequence 19, Application US/09811672
 Patent No. US2002055490A1
 GENERAL INFORMATION:
 APPLICANT: BALL, Tanja
 APPLICANT: VRTALA, Susanne
 APPLICANT: SPERR, Wolfgang
 APPLICANT: VALENT, Peter
 APPLICANT: SUSANI, Markus
 APPLICANT: KRAFT, Dietrich
 APPLICANT: VALENTE, Rudolf
 APPLICANT: LAFER, Sylvia
 TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT MOLECULES, VECTORS, AND HOSTS CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS
 TITLE OF INVENTION: THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS
 FILE REFERENCE: 1614-0247P
 CURRENT APPLICATION NUMBER: US/09/811,672
 CURRENT FILING DATE: 2001-03-20
 NUMBER OF SEQ ID NOS: 28
 SEQ ID NO 19
 LENGTH: 13
 TYPE: PRT
 ; ORGANISM: Timothy Grass
 ; US-09-811-672-19

Query Match 32.8%; Score 22; DB 9; Length 13;
 Best Local Similarity 50.0%; Pred. No. 3.2e+03; 2; Mismatches 1; Indels 0; Gaps 0; Matches 0;

QY 3 EQVSPY 8
 Db 1 EPIAPY 6

RESULT 15
 US-09-946-175-8
 Sequence 8, Application US/09946175
 Patent No. US2002010667A1
 GENERAL INFORMATION:
 APPLICANT: Warner-Lambert
 TITLE OF INVENTION: IDENTIFICATION OF A CAPACITATIVE CALCIUM CHANNEL IN ANTIGEN PRESENTING CELLS AND USES THEREOF
 FILE REFERENCE: M161(310800)

RESULT 13

```
; CURRENT APPLICATION NUMBER: US/09/946,175
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-946-175-8

Query Match 32.8%; Score 22; DB 9; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.2e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0;
Ov 5 VSPYTLKG 13
Qy  : | | :: | 0;
Db 4 LGPYVMMIG 12
```

Search completed: October 1, 2004, 13:49:24
Job time : 46 secs

John

Smith

| | | | | | |
|--|---------------------------------|--------------------|-------|-------------|----------|
| Copyright (c) 1993 - 2004 Compugen ltd. | GenCore version 5.1.6 | | | | |
| OM protein - protein search, using sw model | | | | | |
| Run on: October 1, 2004, 13:46:58 ; Search time 51 Seconds | (without alignments) | | | | |
| | 7.2022 Million cell updates/sec | | | | |
| Title: US-09-674-616A-2 | | | | | |
| Perfect score: 67 | | | | | |
| Sequence: 1 NOEQVSPYTLKG 13 | | | | | |
| Scoring table: BLOSUM62 | | | | | |
| Gapext 0.5 | | | | | |
| Searched: 1586107 seqs, 282547505 residues | | | | | |
| Total number of hits satisfying chosen parameters: | 15593 | | | | |
| Minimum DB seq length: 13 | | | | | |
| Maximum DB seq length: 13 | | | | | |
| Post-processing: Minimum Match 0% Maximum Match 100% | | | | | |
| Listing first 45 summaries | | | | | |
| Database : A_Geneseq_29Jan04:* | | | | | |
| 1: geneseq1990s:* | | | | | |
| 2: geneseq1990s:* | | | | | |
| 3: geneseq2000s:* | | | | | |
| 4: geneseq2001s:* | | | | | |
| 5: geneseq2002s:* | | | | | |
| 6: geneseq2003as:* | | | | | |
| 7: geneseq2003bs:* | | | | | |
| 8: geneseq2004s:* | | | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | |
| SUMMARIES | | | | | |
| Result No. | Score | Query Match Length | DB ID | Description | |
| 1 | 67 | 100.0 | 13 | 3 | AY67835 |
| 2 | 64 | 95.5 | 13 | 3 | AY67837 |
| 3 | 61 | 91.0 | 13 | 3 | AY67836 |
| 4 | 61 | 91.0 | 13 | 3 | AY67842 |
| 5 | 59 | 88.1 | 13 | 3 | AY67841 |
| 6 | 59 | 88.1 | 13 | 3 | AY67840 |
| 7 | 46 | 68.7 | 13 | 3 | AY67844 |
| 8 | 36 | 53.7 | 13 | 5 | AM50298 |
| 9 | 36 | 53.7 | 13 | 6 | ABG13917 |
| 10 | 27 | 40.3 | 13 | 2 | AYV0946 |
| 11 | 26 | 38.8 | 13 | 2 | AYV0240 |
| 12 | 25 | 37.3 | 13 | 2 | AYE4972 |
| 13 | 25 | 37.3 | 13 | 2 | AWB8008 |
| 14 | 25 | 37.3 | 13 | 5 | AEE3145 |
| 15 | 24 | 35.8 | 13 | 2 | ARR4779 |
| 16 | 24 | 35.8 | 13 | 5 | ABJ00698 |
| 17 | 24 | 35.8 | 13 | 5 | AGG33559 |
| 18 | 24 | 35.8 | 13 | 5 | ABR9726 |
| 19 | 24 | 35.8 | 13 | 5 | ABB7727 |
| 20 | 23 | 34.3 | 13 | 2 | ARR49912 |
| 21 | 23 | 34.3 | 13 | 2 | ARR49915 |
| 22 | 23 | 34.3 | 13 | 2 | ARR49913 |
| 23 | 23 | 34.3 | 13 | 2 | ARR60824 |
| 24 | 23 | 34.3 | 13 | 2 | ARR83958 |
| 25 | 23 | 34.3 | 13 | 5 | AAW06266 |

| | |
|--|--|
| CC | detectable moiety can also act as substrates for Factor XIIIa. The invention relates to compounds which can be used in the diagnosis of thrombosis or embolism and also for diagnosing atherosclerosis, inflammation or cancer. The peptide forms part of the compound |
| CC | XX |
| SQ | Sequence 13 AA; |
| RESULT 2 | Query Match 100.0%; Score 67; DB 3; Length 13; Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 1 NOEQVSPYTLKG 13 |
| AY67837 | AAV67837 standard; peptide; 13 AA. |
| XX | AC AAY67837; |
| XX | 25-APR-2000 (first entry) |
| XX | Alpha-2 antiplasmin enzyme derived peptide #4. |
| XX | Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer; embolism; thrombosis; inflammation; atherosclerosis; diagnosis. |
| XX | Synthetic. |
| XX | Key |
| FH | Location/Qualifiers |
| FT | Modified-site 1 /note= "N-terminal acetyl" |
| FT | XX |
| PN | W0960018-A1. |
| XX | XX |
| PD | 25-NOV-1999. |
| XX | PR 14-MAY-1999; 99WO-GB001550. |
| XX | XX |
| PA | (AMSH) NYCOMED AMERSHAM PLC. |
| XX | XX |
| PT | Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B; Wilson IA, Knox P; |
| XX | XX |
| DR | WPI; 2000-126380/11. |
| XX | PT Novel synthetic analogues for diagnosis of thrombosis, embolism, atherosclerosis, inflammation or cancer. |
| PS | XX |
| XX | Example 2; Page 16; 46pp; English. |
| CC | This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2 antiplasmin is a substrate for the fibrin stabilising enzyme Factor XIIIa. Synthetic analogues of lysine and glutamine labelled with a detectable moiety can also act as substrates for Factor XIIIa. The invention relates to compounds which can be used in the diagnosis of thrombosis or embolism and also for diagnosing atherosclerosis, inflammation or cancer. The peptide forms part of the compound |
| SQ | Sequence 13 AA; |
| Query Match 91.0%; Score 61; DB 3; Length 13; Best Local Similarity 92.3%; Pred. No. 0.00016; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Db 1 NOEQVSPYTLKG 13 | |
| RESULT 4 | AY67842 AAV67842 standard; peptide; 13 AA. |
| XX | AC AAY67842; |
| XX | 25-APR-2000 (first entry) |
| XX | Alpha-2 antiplasmin enzyme derived peptide #9. |
| XX | Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer; embolism; thrombosis; inflammation; atherosclerosis; diagnosis. |
| OS | Synthetic. |
| RESULT 3 | Query Match 100.0%; Score 67; DB 3; Length 13; Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 1 NOEQVSPYTLKG 13 |
| AY67836 | AAV67836 standard; peptide; 13 AA. |
| XX | AC AAY67836; |
| XX | 25-APR-2000 (first entry) |
| XX | Alpha-2 antiplasmin enzyme derived peptide #3. |
| XX | Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer; embolism; thrombosis; inflammation; atherosclerosis; diagnosis. |
| XX | Synthetic. |
| XX | Key |
| FH | Location/Qualifiers |
| FT | Modified-site 1 /note= "N-terminal acetyl" |
| FT | XX |
| PN | W0960018-A1. |
| XX | XX |
| PD | 25-NOV-1999. |
| XX | PR 15-MAY-1998; 98EP-00303872. |
| XX | XX |
| PA | (AMSH) NYCOMED AMERSHAM PLC. |
| XX | XX |
| PT | Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B; Wilson IA, Knox P; |
| XX | XX |
| DR | WPI; 2000-126380/11. |
| XX | PT Novel synthetic analogues for diagnosis of thrombosis, embolism, atherosclerosis, inflammation or cancer. |
| PS | XX |
| XX | Example 2; Page 16; 46pp; English. |
| CC | This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2 antiplasmin is a substrate for the fibrin stabilising enzyme Factor XIIIa. Synthetic analogues of lysine and glutamine labelled with a detectable moiety can also act as substrates for Factor XIIIa. The invention relates to compounds which can be used in the diagnosis of thrombosis or embolism and also for diagnosing atherosclerosis, inflammation or cancer. The peptide forms part of the compound |
| SQ | Sequence 13 AA; |
| Query Match 91.0%; Score 61; DB 3; Length 13; Best Local Similarity 92.3%; Pred. No. 0.00016; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Db 1 NOEQVSPYTLKG 13 | |
| RESULT 4 | AY67842 AAV67842 standard; peptide; 13 AA. |
| XX | AC AAY67842; |
| XX | 25-APR-2000 (first entry) |
| XX | Alpha-2 antiplasmin enzyme derived peptide #9. |
| XX | Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer; embolism; thrombosis; inflammation; atherosclerosis; diagnosis. |
| OS | Synthetic. |
| Query Match 95.5%; Score 64; DB 3; Length 13; Best Local Similarity 92.3%; Pred. No. 4.3e-05; Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Db 1 NOEQVSPYTLKG 13 | |
| RESULT 4 | AY67842 AAV67842 standard; peptide; 13 AA. |
| XX | AC AAY67842; |
| XX | 25-APR-2000 (first entry) |
| XX | Alpha-2 antiplasmin enzyme derived peptide #9. |
| XX | Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer; embolism; thrombosis; inflammation; atherosclerosis; diagnosis. |
| OS | Synthetic. |

XX
PS Example 2; Page 16; 46pp; English.
XX
CC This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
CC detectable moiety can also act as substrates for Factor XIIIa. The
CC invention relates to compounds which can be used in the diagnosis of
CC thrombosis or embolism and also for diagnosing atherosclerosis,
CC inflammation or cancer. The peptide forms part of the compound
XX
SQ Sequence 13 AA;
Query Match 88.1%; Score 59; DB 3; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.00038; ID AAM50298
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NQEQVSPYVLLKG 13
Db 1 NQEQVSPYVLLKG 13
RESULT 7
ID AAY67844
AC AAY67844;
XX DT 25-APR-2000 (first entry)
XX DE Alpha-2 antiplasmin enzyme derived peptide #11.
XX DE Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
OS Synthetic.
XX PN WO9960018-A1.
XX PD 25-NOV-1999.
XX PP 14-MAY-1999; 99WO-GB001550.
XX PR 15-MAY-1998; 98EP-00303872.
XX PA (AMSH) NYCOMED AMERSHAM PLC.
XX PI Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B,
XX PT Wilson IA, Knox P; DR WI; 2000-126380/11.
XX PR Novel synthetic analogues for diagnosis of thrombosis, embolism,
PT atherosclerosis, inflammation or cancer.
XX PS Example 2; Page 17; 46pp; English.
XX
CC This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
CC detectable moiety can also act as substrates for Factor XIIIa. The
CC invention relates to compounds which can be used in the diagnosis of
CC thrombosis or embolism and also for diagnosing atherosclerosis,
CC inflammation or cancer. The peptide forms part of the compound
XX
SQ Sequence 13 AA;
Query Match 68.7%; Score 46; DB 3; Length 13;
Best Local Similarity 69.2%; Pred. No. 0.11; ID AAM50298
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 NQEQVSPYVLLKG 13
Db 1 NQEQVSPYVLLKG 13
RESULT 8
ID AAM50298
AC AAM50298;
XX DT 04-FEB-2002 (first entry)
XX DE Factor XIIIa substrate-polylsine peptide chimera.
XX KW Tissue engineering; tissue repair; tissue regeneration; drug delivery;
KW Factor XIIIa; heparin.
XX OS Synthetic.
XX FH Key location/Qualifiers
FT Modified-site I
FT /note= "dansyl leucine, allows detection of peptide by
FT Peptide fluorescence"
FT /note= "Factor XIIIa substrate"
FT 2.8
FT 9.13
FT /note= "heparin-binding peptide"
XX PN WO200183522-A2.
XX PD 08-NOV-2001.
XX PR 01-MAY-2000; 2000WO-US011947.
XX PR 01-MAY-2000; 2000WO-US011947.
XX PA (BIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
PA (HUBB-) HUBBELL J A.
XX PI Hubbell JA, Schense JC, Sakiyama-Elbert SE;
XX DR WPI; 2002-041479/05.
XX PT Novel growth factor modified protein matrix useful for tissue repair,
PT regeneration and/or remodeling, and/or drug delivery.
XX
PS Example 2; Page 25; 51pp; English.
XX
CC The present sequence is that of a fluorescent synthetic peptide, which
CC has a Factor XIIIa substrate at the N-terminal end and a polylysine
CC moiety at the C-terminus. The Peptide is used to produce a heparin-
CC peptide chimera by coupling to a heparin oligosaccharide, with a unique
CC aldehyde group on one end, via reductive amination. A matrix is formed in
CC which heparin is used to incorporate heparin-binding growth factors for
use in tissue repair, regeneration, remodeling, remodeling, and/or drug delivery. The
CC invention provides biocompatible and biodegradable matrices incorporating
CC bioactive proteins such as growth factors. The matrices can be formed in
CC vitro or in vivo at the site of implantation, and provide controlled
CC and/or sustained release of the bioactive protein.
XX
SQ Sequence 13 AA;
Query Match 53.7%; Score 36; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2; ID ABG73917
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NQEQVSP 7
Db 2 NQEQVSP 8
RESULT 9
ID ABG73917
ABG73917 standard; peptide; 13 AA.

XX ABG73917;
 AC AC AAY20946;
 XX XX
 DT DT 22-JUL-1999 (first entry)
 XX XX
 DE Human presenilin II mutant protein fragment 39.
 XX Human; beta-amyloid precursor protein; beta APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GfAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell Leukemia/lymphoma 2 proto-oncogene; HmGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN WO9843322-A2.
 XX XX
 PD 15-OCT-1998.
 XX XX
 PR 02-APR-1998; 98WO-1B000705.
 XX XX
 PA 10-APR-1997; 97US-0043163P.
 XX XX
 PA (ROYA-) ROYAL NETHERLANDS ACADEMIA ARTS & SCI.
 PA (TURK-) RIJKSUNIVERSITEIT Utrecht.
 XX XX
 PT Van Leeuwen FW, Grosveld FG, Burbach JPH;
 DR MPA; 1998-609901/51.
 XX DR N-PSDB; AAX/5762.
 XX PT Diagnosing disease by detecting frameshift mutations in RNA or
 PS corresponding protein mutations - used to diagnose cancer and
 XX neurological diseases, particularly Alzheimer's disease, and also for
 CC treatment and prevention with specific ribozymes or wild-type RNA.
 CC Disclosure; Fig 11; 258pp; English.
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (Map2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GfAP), the cellular tumour antigen p53, B-cell Leukemia/lymphoma
 CC protein (HmGP-C) and neuroendocrine specific protein A.
 XX Sequence 13 AA;
 Query Match 53.7%; Score 36; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.2; Mismatches 7; Conservative 0; Indels 0; Gaps 0;
 Matches 2; NQEQVSP 8
 QY 1 NQEQVSP 7
 QY 2 NQEQVSP 8
 RESULT 10 AAY20946 standard; protein; 13 AA.
 ID AAY20946

| Key | Location/Qualifiers |
|-----------------------|--|
| Region | 6 . .9 /note= "PPPPY motif" |
| PT | 19-SEP-2001; 2001WO-IR001914. |
| XX | XX |
| PN | W0937223-A1. |
| PD | 09-OCT-1997. |
| XX | XX |
| PF | 03-APR-1997; 97WO-US005547. |
| XX | XX |
| PR | 03-APR-1996; 96US-00630916. |
| XX | XX |
| PA | (CYTO-) CYTOGEN CORP. |
| PA | (UNNC-) UNIV NORTH CAROLINA. |
| XX | XX |
| PI | Pirozzi G, Kay BK, Fowlkes DM; |
| XX | XX |
| DR | WPI; 1997-50334/46. |
| XX | XX |
| PT | Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are useful in targetted drug selection. |
| PT | XX |
| PS | Claim 92; Fig 27; 220pp; English. |
| XX | XX |
| CC | Peptides AAW8005-08 are the sequences of WW domain binding clones obtained by screening random or biased libraries with the WW domains of the novel WWP proteins. The present peptide was obtained after screening with WW domain 1 of WWP1 (WWP1.1). The peptides are peptide recognition units ("ligands"), and are used for analysing specificities of the WW domains. The WW domain is a small functional domain. Its name is derived from the observation that two tryptophan residues, one in the amino terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling and growth regulation or the organisation of the cytoskeleton. Polypeptides containing a WW domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions. note: ID sequence in SEQ ID listing differs from sequence given in figure. The SEQ ID sequence is as follows: GSEQQPPPYEYTVK |
| CC | XX |
| SQ | Sequence 13 AA; |
| Query Match | 37.3%; Score 25; DB 2; Length 13; |
| Best Local Similarity | 50.0%; Pred. No. 9.8e+02; |
| Matches | 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0; |
| QY | 3 EQVSPYTLK 12 |
| Db | 4 EOPPYETVK 13 |
| RESULT 15 | |
| ID | AAR34779 standard; peptide: 13 AA. |
| XX | XX |
| AC | AAR34779; |
| XX | XX |
| DT | 25-MAR-2003 (revised) |
| DT | 16-JUL-1993 (first entry) |
| XX | XX |
| DE | CAD tryptic peptide, internal sequence 10. |
| XX | XX |
| KW | Tobacco; cinnamyl alcohol dehydrogenase; CAD; tryptic peptide; subunit; probe; primer; plant; lignin; biosynthesis; biosynthesis; digestibility; feed; cellulose; crop; pathogen; timber. |
| XX | XX |
| OS | Nicotiana tabacum. |
| XX | XX |
| PN | W09305159-A1. |
| XX | XX |
| DD | 18-MAR-1993. |
| XX | XX |
| PF | 27-APR-1992; 92WO-GB0000774. |
| XX | XX |
| PR | 26-APR-1991; 91GB-00009063. |
| XX | XX |
| PA | (ICIL) IMPERIAL CHEM IND PLC. |
| XX | XX |
| PT | Boudet AM, Inze DG, Schuch WW; |
| XX | XX |
| DR | WPI; 1993-100982/12. |
| XX | XX |
| DE | Influenza A virus subtype 16 haemagglutinin (HA) protein fragment #9. |
| XX | XX |
| KW | Haemagglutinin; HA protein; vaccine; infection. |
| XX | XX |
| OS | Influenza A virus. |
| XX | XX |
| PN | WO200224734-A2. |
| PD | 28-MAR-2002. |
| XX | XX |
| PT | Modifying lignin content of plants - comprises use of recombinant DNA encoding lignin biosynthetic enzyme, e.g. CAD. |
| XX | XX |
| PS | Disclosure; Fig 1; 69pp; English. |
| XX | XX |
| CC | The sequences given in AAR34768-82 represent peptide sequences derived from tobacco cinnamyl alcohol dehydrogenase (CAD) tryptic peptides. Purified CAD consists of two subunits of approximate molecular weight |
| CC | XX |

42.5 kD and 44 kD. These peptides were derived by trypsin digestion of both polypeptides. These peptides were used to produce probes and primers which were used in the isolation of the CAD cDNA. The CAD cDNA may be used in the production of a recombinant DNA comprising a gene which is essential to plant lignin biosynthesis. When incorporated into a plant genome by transformation, mRNA transcribed from the coding region inhibits production of the enzyme from the endogenous gene. The recombinant DNA may be used to provide plants having altered ability to synthesize lignin. The principle applications of altered lignin biosynthesis are improvement of digestibility of animal forage crops, reduction of lignin in woody feedstocks for cellulose fibre extraction, improvement of the response of crop plants to pathogen attack and improvement of timber quality. (Updated on 25-MAR-2003 to correct PN field.)

XX

Sequence 13 AA:

Query Match 35.8%; Score 24; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.5e+03; 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 5 VSPYT 9
:|||
Db 5 LSPYT 9

Search completed: October 1, 2004, 13:47:59
Job time : 54 secs